

Qualitative Comparative Analysis (QCA) Using R: A Beginner's Guide

Independent Exercise on a full QCA - Solution

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Contents

1. BEFORE THE ANALYTIC MOMENT	1
2. NECESSITY ANALYSIS FOR THE PRESENCE OF THE OUTCOME	2
3. SUFFICIENCY ANALYSIS FOR THE PRESENCE OF THE OUTCOME	7
Truth Table	7
Logical Minimization	8
4. NECESSITY ANALYSIS FOR THE ABSENCE OF THE OUTCOME	12
5. SUFFICIENCY ANALYSIS FOR THE ABSENCE OF THE OUTCOME	13
Truth Table	13
Logical Minimization	14
6. ENHANCED STANDARD ANALYSIS FOR THE ABSENCE OF THE OUT- COME	16
Assumptions contradicting necessity	16
Contradictory easy counterfactuals	18
Simultaneous subset relations	19
Impossible remainders	19
7. THEORY EVALUATION	20
8. ROBUSTNESS	22
Sensitivity ranges:	22
Creating the test solutions:	23
Calculate robustness fit parameters:	24
Identify types of robustness relevant cases and robustness case parameters:	24
9. SMMR Y	25
10. SMMR $\sim Y$	26
11. CLUSTER $\sim Y$	27

1. BEFORE THE ANALYTIC MOMENT

Load the packages:

```
library(SetMethods)
library(QCA)
```

The data comes from Paykani, Toktam, Rafiey, Hassan, Sajjadi, Homeira (2018) "A fuzzy set qualitative comparative analysis of 131 countries: Which configuration of the structural conditions can explain health better?" [<https://pubmed.ncbi.nlm.nih.gov/29357889/>]

Outcome: HL = High life expectancy

Conditions:

HE = High quality education GG = Good governance AH = Affluent health system HI = High income inequality HW = High wealth

Load the data:

```
data("PAYF")
head(PAYF)
```

```
##      COUNTRY                REGION  HE  GG  AH  HI  HW  HL  LL
## ALB  Albania          European Region 0.33 0.47 0.32 0.14 0.41 0.84 0.16
## AGO  Angola            African Region 0.00 0.00 0.04 1.00 0.13 0.00 1.00
## ARG  Argentina Region of the Americas 0.82 0.36 0.68 0.93 0.78 0.67 0.33
## ARM  Armenia          European Region 0.32 0.42 0.68 0.02 0.20 0.46 0.54
## AUS  Australia Western Pacific Region 1.00 0.99 0.99 0.11 0.99 0.99 0.01
## AUT  Austria          European Region 0.99 0.99 1.00 0.04 1.00 0.98 0.02
```

Store condition names in one object in order to save time and space:

```
conds <- c("HE", "GG", "AH", "HI", "HW")
```

The data is already calibrated, therefore we can perform some diagnostics tests

Check the skewness of the data for the 5 conditions and the outcome HL:

```
skew.check(PAYF[, 3:8])
```

```
## [1] "Set HE - Cases > 0.5 / Total number of cases: 58 / 131 = 44.27 %"
## [2] "Set GG - Cases > 0.5 / Total number of cases: 64 / 131 = 48.85 %"
## [3] "Set AH - Cases > 0.5 / Total number of cases: 56 / 131 = 42.75 %"
## [4] "Set HI - Cases > 0.5 / Total number of cases: 65 / 131 = 49.62 %"
## [5] "Set HW - Cases > 0.5 / Total number of cases: 64 / 131 = 48.85 %"
## [6] "Set HL - Cases > 0.5 / Total number of cases: 52 / 131 = 39.69 %"
```

Check whether there are any ambiguous cases with set-membership scores of 0.5 in any of the 5 conditions and the outcome HL:

```
ambig.cases(PAYF[, 3:8])
```

```
## [1] "There are no cases with fuzzy-set scores of 0.5."
```

2. NECESSITY ANALYSIS FOR THE PRESENCE OF THE OUTCOME

Check whether we have any single necessary conditions for outcome HL:

```
QCAfit(PAYF[, 3:7],
        PAYF$HL,
        necessity = TRUE)
```

```
##      Cons.Nec Cov.Nec  RoN
## HE      0.885   0.800 0.845
## GG      0.858   0.761 0.815
## AH      0.790   0.756 0.833
## HI      0.433   0.383 0.629
## HW      0.897   0.799 0.841
## ~HE     0.338   0.280 0.560
## ~GG     0.342   0.288 0.571
## ~AH     0.382   0.300 0.540
## ~HI     0.704   0.595 0.702
## ~HW     0.340   0.285 0.568
```

Display SUIN conditions, setting the inclusion cutoff to 0.9, coverage cutoff to 0.6, and RoN to 0.5. Display only the combinations of a maximum of two conditions.

```
SUIN_y <- superSubset(data = PAYF,  
  outcome = "HL",  
  conditions = conds,  
  incl.cut = 0.9,  
  cov.cut = 0.6,  
  ron.cut = 0.5,  
  depth = 2)
```

SUIN_y

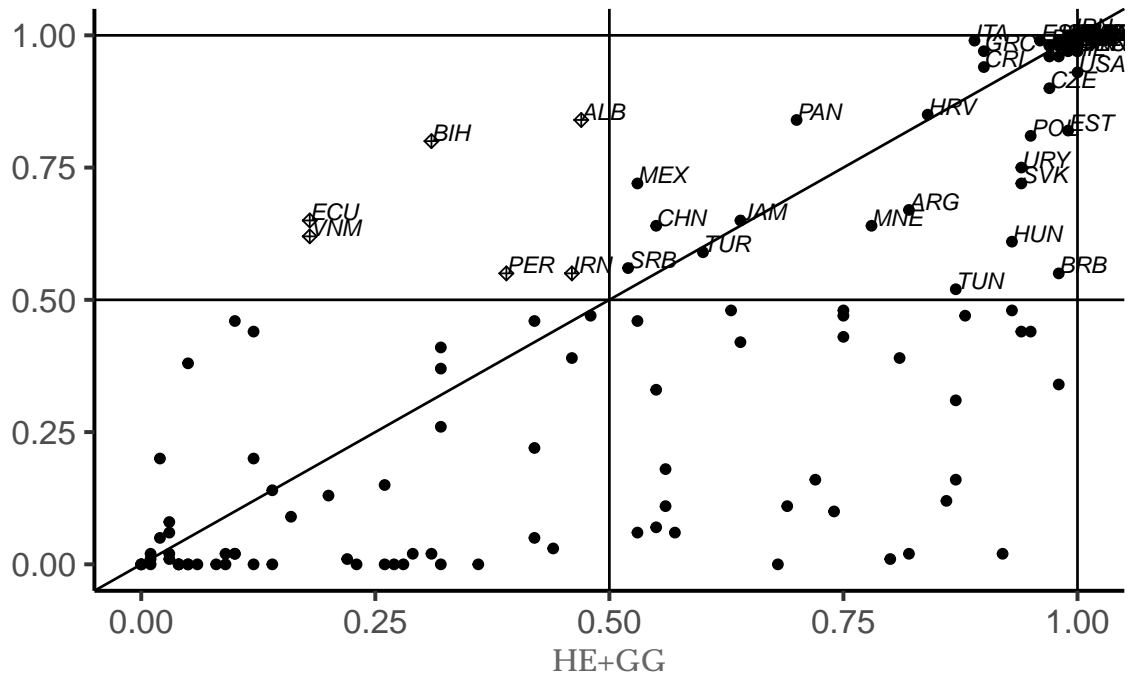
```
##  
##          inclN   RoN   covN  
## -----  
## 1 HE+GG  0.923  0.732  0.712  
## 2 HE+AH  0.906  0.748  0.719  
## 3 HE+~HI 0.924  0.595  0.621  
## 4 HE+HW  0.928  0.774  0.747  
## 5 GG+AH  0.906  0.698  0.680  
## 6 GG+HW  0.934  0.732  0.716  
## 7 AH+HW  0.916  0.751  0.724  
## 8 ~HI+HW 0.941  0.577  0.618  
## -----
```

Plot the results:

```
pimplot(data = PAYF,  
  outcome = "HL",  
  results = SUIN_y,  
  necessity = TRUE)
```

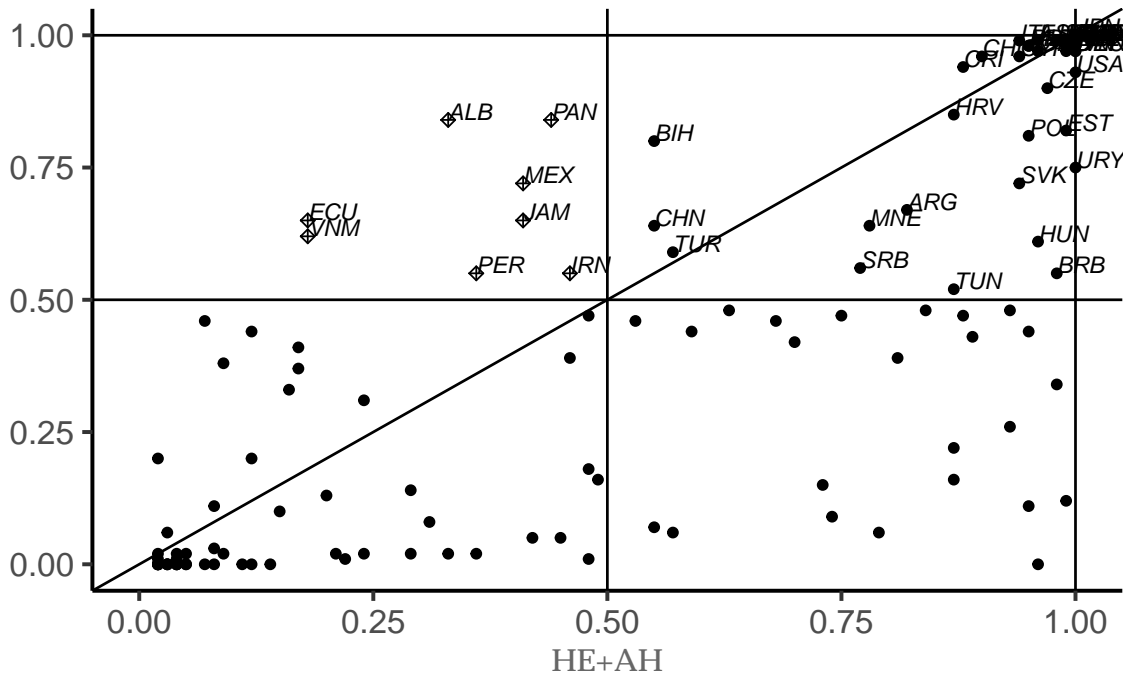
NECESSITY PLOT

Cons.Nec: 0.923; Cov.Nec: 0.712; RoN: 0.732



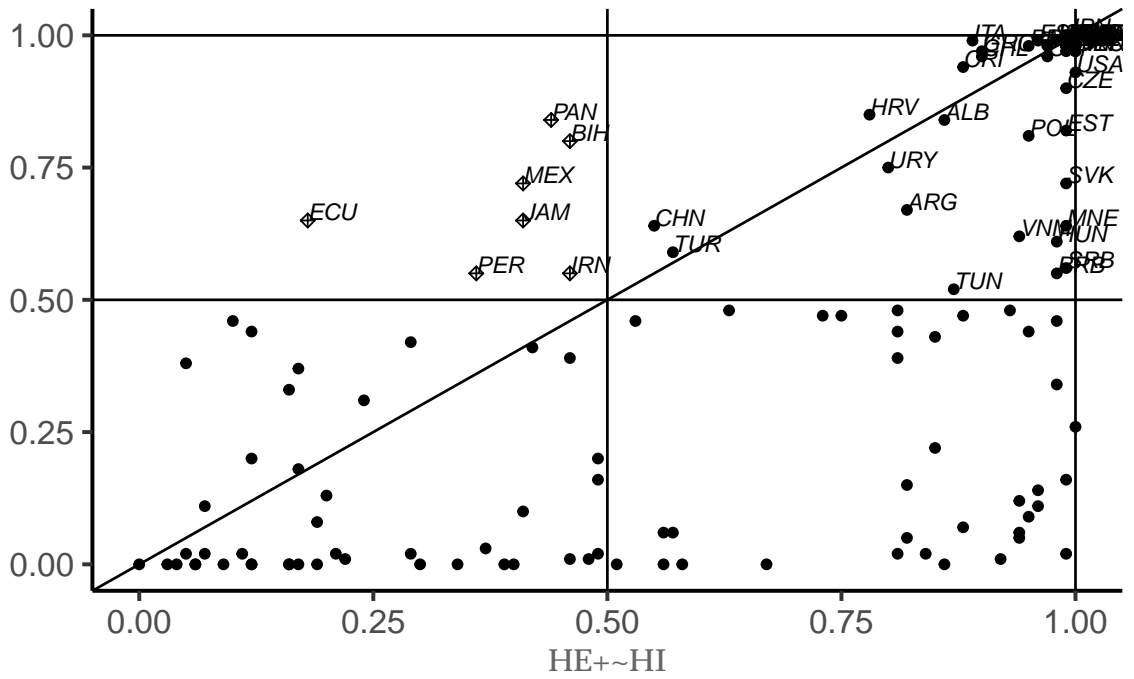
NECESSITY 100

Cons.Nec: 0.906; Cov.Nec: 0.719; RoN: 0.748



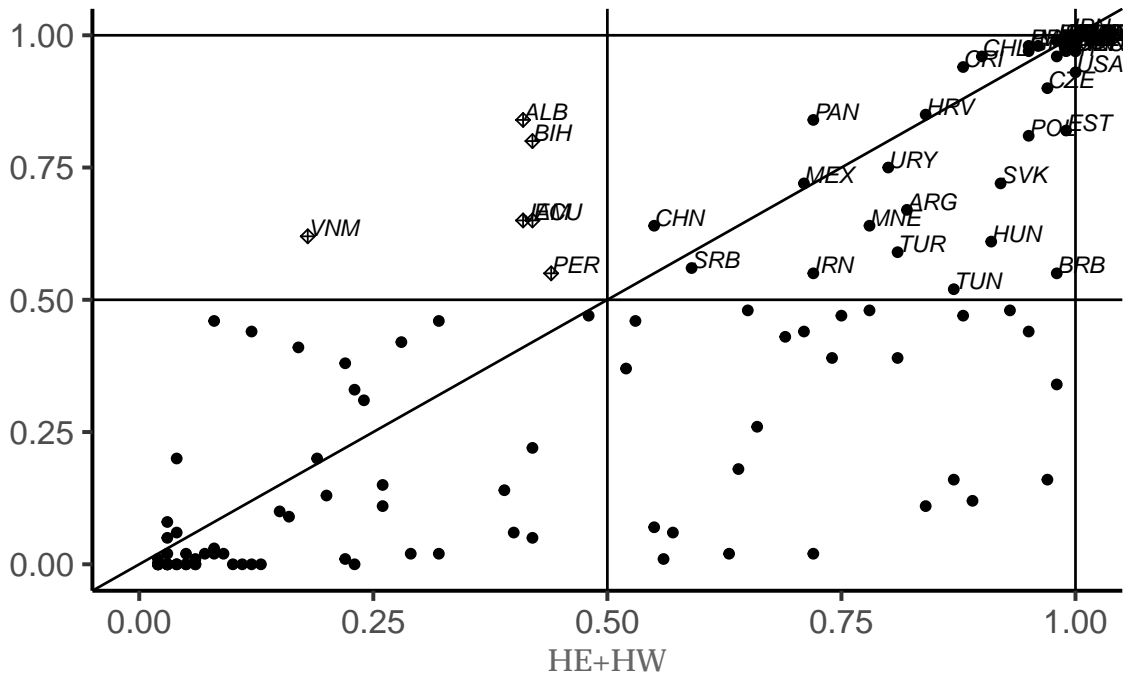
NECESSITY 100

Cons.Nec: 0.924; Cov.Nec: 0.621; RoN: 0.595



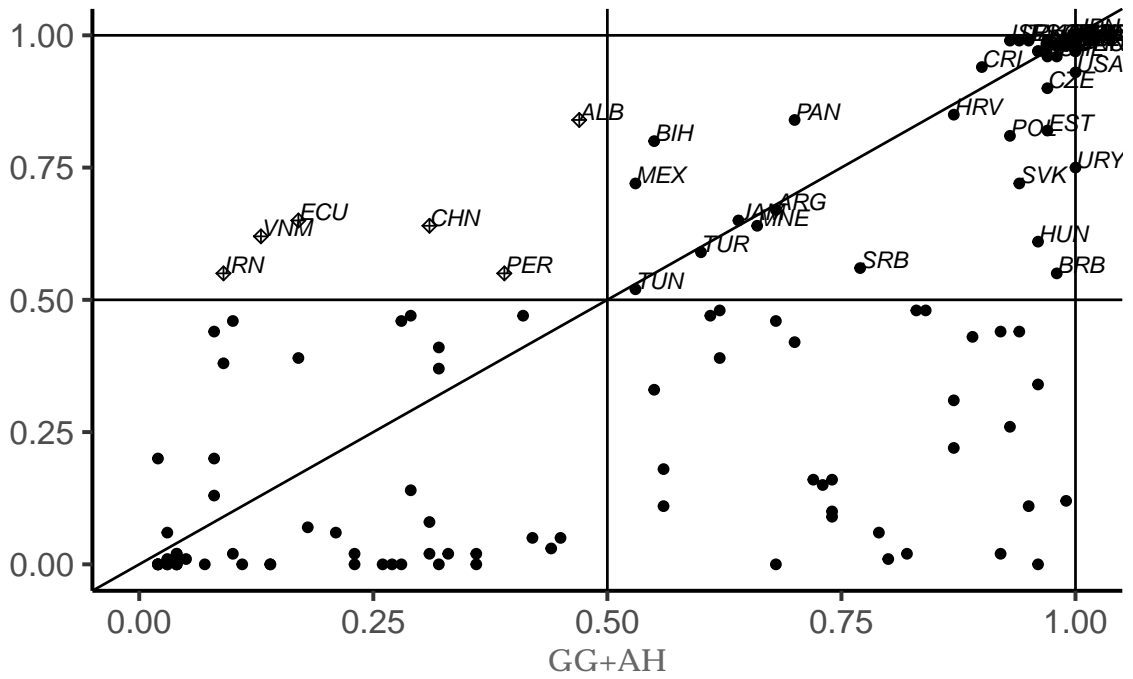
NECESSITY 100

Cons.Nec: 0.928; Cov.Nec: 0.747; RoN: 0.774



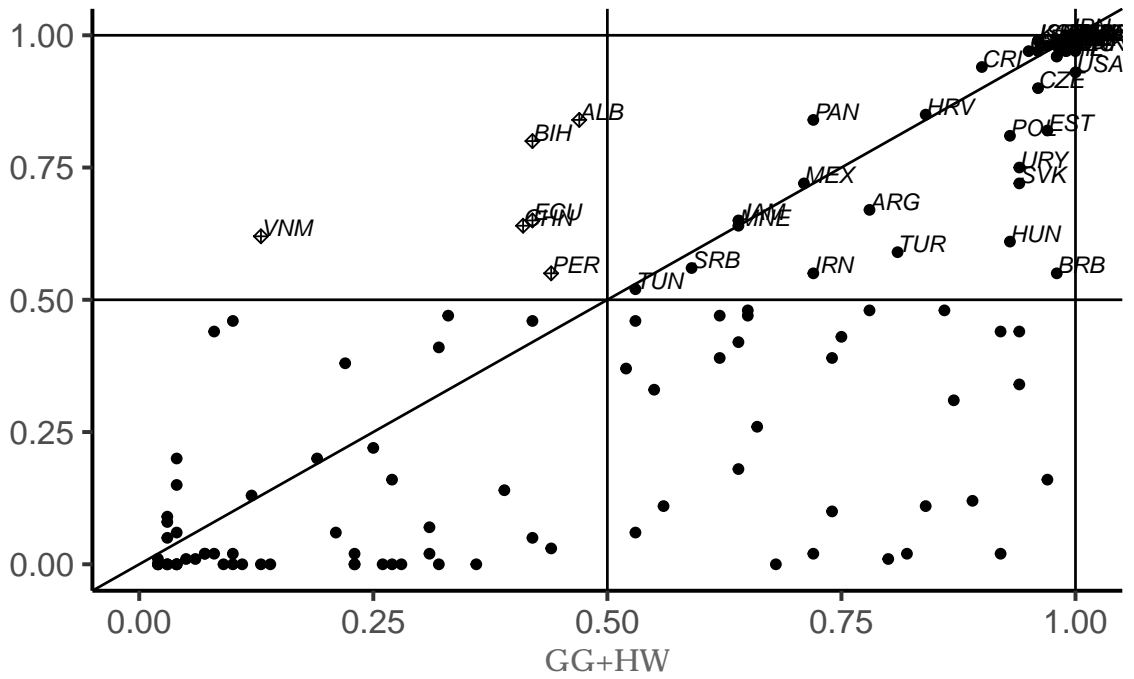
NECESSITY 100

Cons.Nec: 0.906; Cov.Nec: 0.680; RoN: 0.698



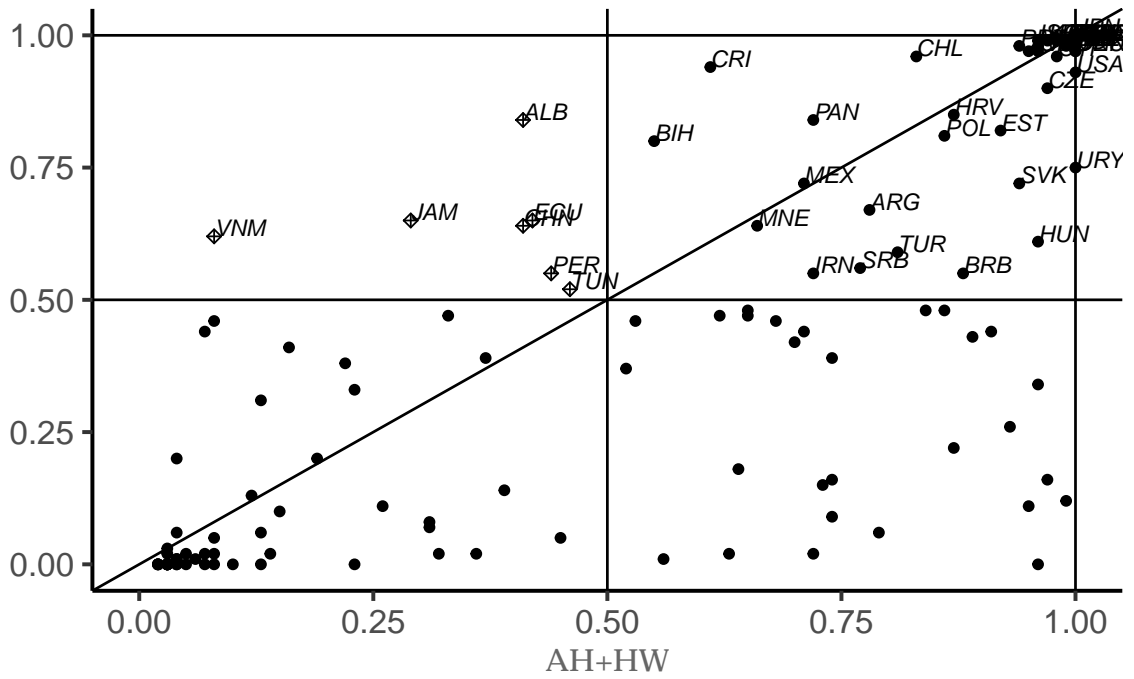
NECESSITY 100

Cons.Nec: 0.934; Cov.Nec: 0.716; RoN: 0.732



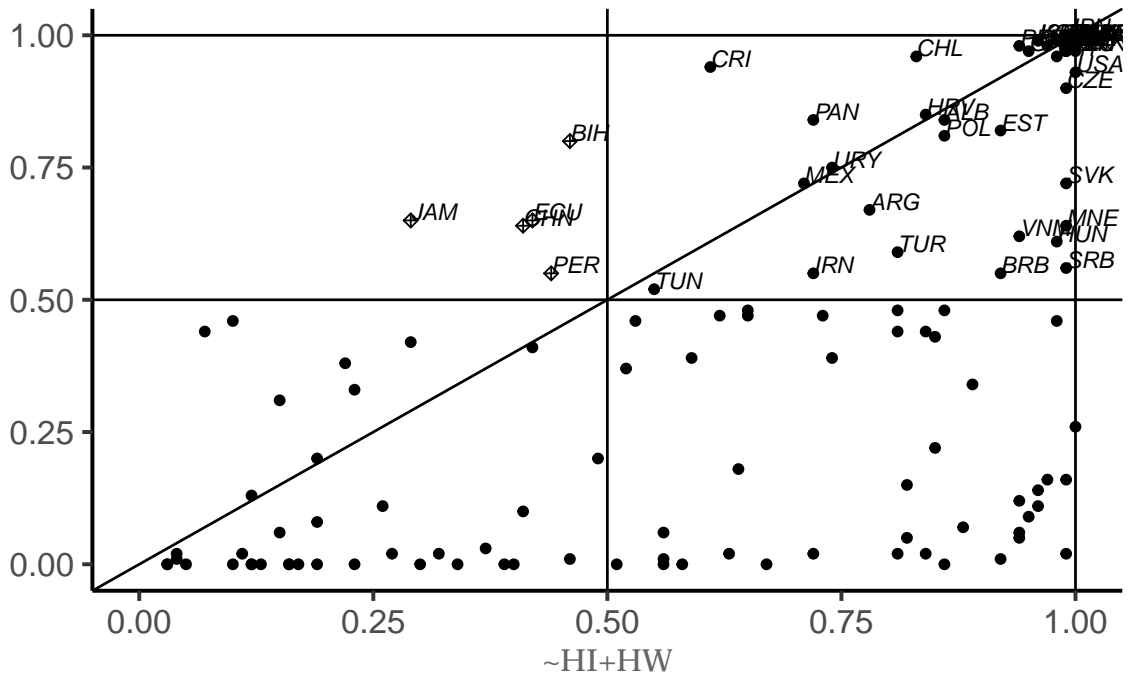
NECESSITY 100

Cons.Nec: 0.916; Cov.Nec: 0.724; RoN: 0.751



NECESSITY PLOT

Cons.Nec: 0.941; Cov.Nec: 0.618; RoN: 0.577



3. SUFFICIENCY ANALYSIS FOR THE PRESENCE OF THE OUTCOME

Truth Table

Create the truth table, setting the inclusion cutoff to 0.84 and the number of cases needed to include a row in the minimization to 1.

```
TT_y <- truthTable(data = PAYF,
  outcome = "HL",
  conditions = conds,
  incl.cut = 0.84,
  n.cut = 1,
  sort.by = c("OUT", "incl"),
  complete = TRUE,
  show.cases = FALSE)
```

TT_y

```
##
##   OUT: output value
##   n: number of cases in configuration
##   incl: sufficiency inclusion score
##   PRI: proportional reduction in inconsistency
##
##   HE GG AH HI HW   OUT   n  incl  PRI
## 30  1  1  1  0  1     1   36 0.929 0.906
## 32  1  1  1  1  1     1    5 0.925 0.824
## 24  1  0  1  1  1     1    2 0.890 0.470
## 20  1  0  0  1  1     1    2 0.873 0.281
## 14  0  1  1  0  1     1    1 0.868 0.435
## 26  1  1  0  0  1     1    1 0.855 0.375
## 13  0  1  1  0  0     1    1 0.850 0.248
## 28  1  1  0  1  1     1    4 0.846 0.525
## 19  1  0  0  1  0     0    2 0.809 0.173
```

```

## 25  1  1  0  0  0    0    2  0.807 0.192
## 15  0  1  1  1  0    0    1  0.806 0.215
## 21  1  0  1  0  0    0    1  0.785 0.145
##  4  0  0  0  1  1    0    4  0.765 0.219
##  6  0  0  1  0  1    0    1  0.755 0.228
## 22  1  0  1  0  1    0    2  0.753 0.209
## 17  1  0  0  0  0    0    1  0.747 0.110
## 12  0  1  0  1  1    0    6  0.734 0.248
##  7  0  0  1  1  0    0    2  0.703 0.151
##  5  0  0  1  0  0    0    4  0.617 0.100
## 11  0  1  0  1  0    0    7  0.537 0.083
##  1  0  0  0  0  0    0   16  0.361 0.060
##  3  0  0  0  1  0    0   30  0.332 0.036
##  2  0  0  0  0  1    ?    0    -    -
##  8  0  0  1  1  1    ?    0    -    -
##  9  0  1  0  0  0    ?    0    -    -
## 10  0  1  0  0  1    ?    0    -    -
## 16  0  1  1  1  1    ?    0    -    -
## 18  1  0  0  0  1    ?    0    -    -
## 23  1  0  1  1  0    ?    0    -    -
## 27  1  1  0  1  0    ?    0    -    -
## 29  1  1  1  0  0    ?    0    -    -
## 31  1  1  1  1  0    ?    0    -    -

```

Logical Minimization

Produce the conservative solution:

```

sol_yc <- minimize(TT_y,
                  details = TRUE)

sol_yc

##
## M1: HE*GG*HW + HE*HI*HW + ~HE*GG*AH*~HI -> HL
##
##          inclS  PRI  covS  covU
## -----
## 1      HE*GG*HW  0.901  0.864  0.800  0.473
## 2      HE*HI*HW  0.862  0.688  0.334  0.043
## 3      ~HE*GG*AH*~HI  0.844  0.373  0.134  0.011
## -----
##          M1  0.885  0.837  0.855

```

Produce the most parsimonious solution:

```

sol_yp <- minimize(TT_y,
                  details = TRUE,
                  include = "?")

sol_yp

##
## M1: ~HE*GG*~HI + HE*GG*HW + HE*HI*HW -> HL
## M2: ~HE*GG*~HI + HE*HI*HW + GG*~HI*HW -> HL
## M3: HE*GG*HW + HE*HI*HW + GG*AH*~HI -> HL
## M4: HE*~AH*HW + HE*AH*HI + GG*AH*~HI -> HL
## M5: HE*~AH*HW + HE*HI*HW + GG*AH*~HI -> HL
## M6: HE*~AH*HW + GG*AH*~HI + AH*HI*HW -> HL
## M7: HE*HI*HW + GG*AH*~HI + GG*~HI*HW -> HL
## M8: HE*HI*HW + GG*AH*~HI + ~AH*~HI*HW -> HL
##
##
## -----

```

```

##          inclS  PRI  covS  covU  (M1)  (M2)  (M3)  (M4)  (M5)  (M6)
## -----
## 1  ~HE*GG*~HI  0.670  0.190  0.151  0.005  0.018  0.014
## 2   HE*GG*HW  0.901  0.864  0.800  0.034  0.472      0.039
## 3  HE*~AH*HW  0.828  0.463  0.270  0.000      0.094  0.006  0.094
## 4   HE*AH*HI  0.908  0.777  0.252  0.002      0.044
## 5   HE*HI*HW  0.862  0.688  0.334  0.000  0.043  0.172  0.043      0.042
## 6   GG*AH*~HI  0.908  0.878  0.631  0.000      0.013  0.452  0.454  0.453
## 7   GG*~HI*HW  0.910  0.879  0.644  0.001      0.440
## 8  ~AH*~HI*HW  0.748  0.266  0.149  0.001
## 9   AH*HI*HW  0.855  0.684  0.251  0.001      0.045
## -----
##          M1  0.848  0.787  0.862
##          M2  0.847  0.782  0.830
##          M3  0.878  0.827  0.857
##          M4  0.882  0.828  0.826
##          M5  0.879  0.825  0.824
##          M6  0.868  0.810  0.827
##          M7  0.880  0.828  0.824
##          M8  0.864  0.805  0.828
## -----
##          (M7)  (M8)
## -----
## 1  ~HE*GG*~HI
## 2   HE*GG*HW
## 3  HE*~AH*HW
## 4   HE*AH*HI
## 5   HE*HI*HW  0.172  0.169
## 6   GG*AH*~HI  0.008  0.453
## 7   GG*~HI*HW  0.007
## 8  ~AH*~HI*HW      0.011
## 9   AH*HI*HW
## -----

```

Check the simplifying assumptions:

```
sol_yp$SA
```

```

## $M1
##   HE GG AH HI HW
## 9  0  1  0  0  0
## 10 0  1  0  0  1
##
## $M2
##   HE GG AH HI HW
## 9  0  1  0  0  0
## 10 0  1  0  0  1
##
## $M3
##   HE GG AH HI HW
## 29 1  1  1  0  0
##
## $M4
##   HE GG AH HI HW
## 18 1  0  0  0  1
## 23 1  0  1  1  0
## 29 1  1  1  0  0
## 31 1  1  1  1  0
##
## $M5

```

```

##      HE GG AH HI HW
## 18  1  0  0  0  1
## 29  1  1  1  0  0
##
## $M6
##      HE GG AH HI HW
##  8  0  0  1  1  1
## 16  0  1  1  1  1
## 18  1  0  0  0  1
## 29  1  1  1  0  0
##
## $M7
##      HE GG AH HI HW
## 10  0  1  0  0  1
## 29  1  1  1  0  0
##
## $M8
##      HE GG AH HI HW
##  2  0  0  0  0  1
## 10  0  1  0  0  1
## 18  1  0  0  0  1
## 29  1  1  1  0  0

```

Produce the intermediate solution with the following directional expectations 1, 1, 1, 0, 1

```

sol_yi <- minimize(TT_y,
                  details = TRUE,
                  include = "?",
                  dir.exp = c(1, 1, 1, 0, 1))
sol_yi

```

```

##
## From C1P1, C1P2:
##
## M1:      HE*GG*HW + HE*HI*HW + ~HE*GG*AH*~HI -> HL
##
##              inclS    PRI    covS    covU
## -----
## 1      HE*GG*HW  0.901  0.864  0.800  0.473
## 2      HE*HI*HW  0.862  0.688  0.334  0.043
## 3      ~HE*GG*AH*~HI  0.844  0.373  0.134  0.011
## -----
##              M1  0.885  0.837  0.855
##
##
## From C1P3, C1P4, C1P5, C1P6, C1P7, C1P8:
##
## M1:      HE*GG*HW + HE*HI*HW + GG*AH*~HI -> HL
##
##              inclS    PRI    covS    covU
## -----
## 1      HE*GG*HW  0.901  0.864  0.800  0.039
## 2      HE*HI*HW  0.862  0.688  0.334  0.043
## 3      GG*AH*~HI  0.908  0.878  0.631  0.013
## -----
##              M1  0.878  0.827  0.857

```

Check the easy counterfactuals

```

sol_yi$i.sol$C1P1$EC

```

```

## [1] V1 V2 V3 V4 V5

```

<0 rows> (or 0-length row.names)

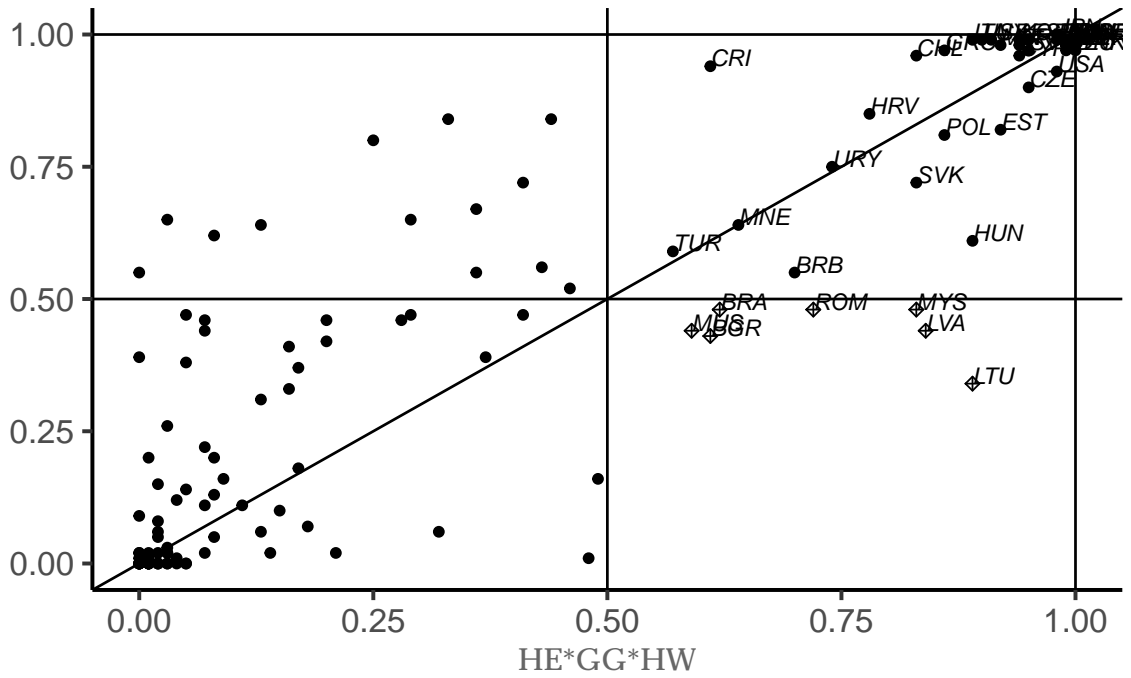
There are no easy counterfactuals

Plot the intermediate solution

```
pimplot(data = PAYF,  
        results = sol_yi,  
        outcome = "HL")
```

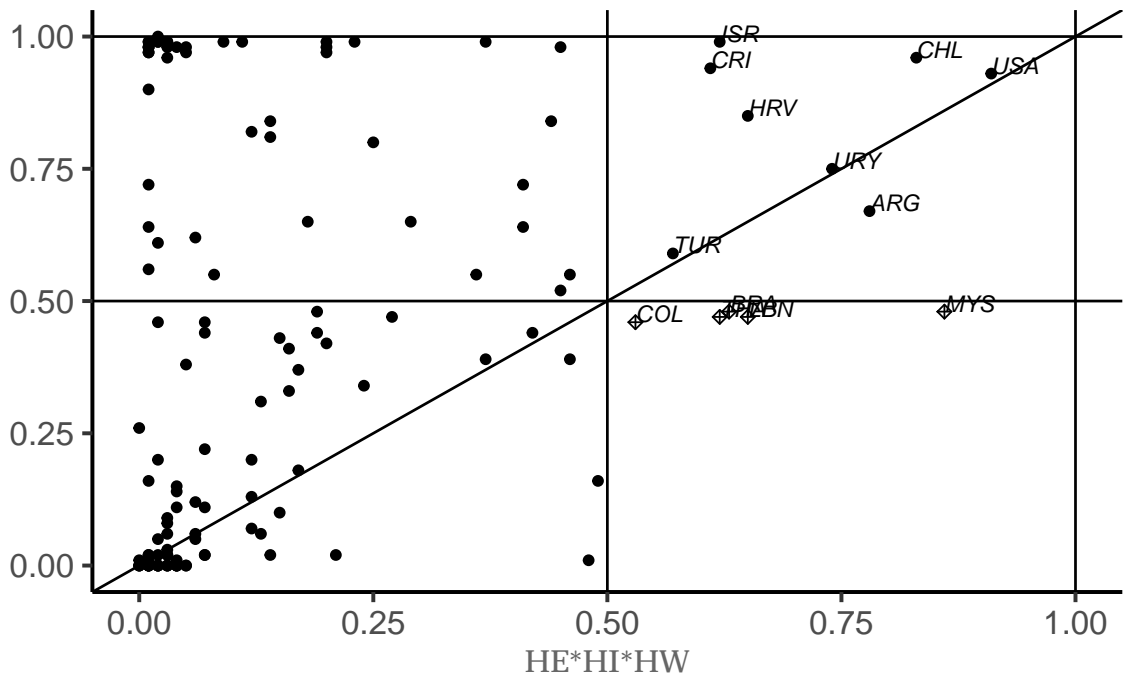
Sufficiency Plot

Cons.Suf: 0.901; Cov.Suf: 0.800; PRI: 0.864



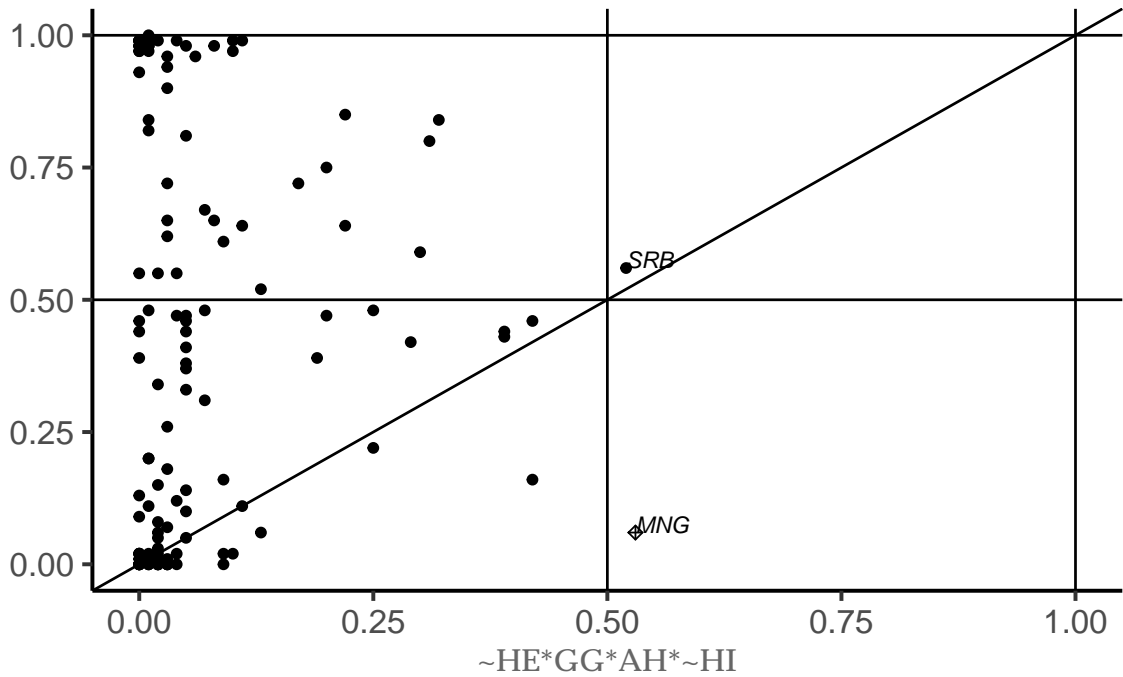
Sufficiency Plot

Cons.Suf: 0.862; Cov.Suf: 0.334; PRI: 0.688



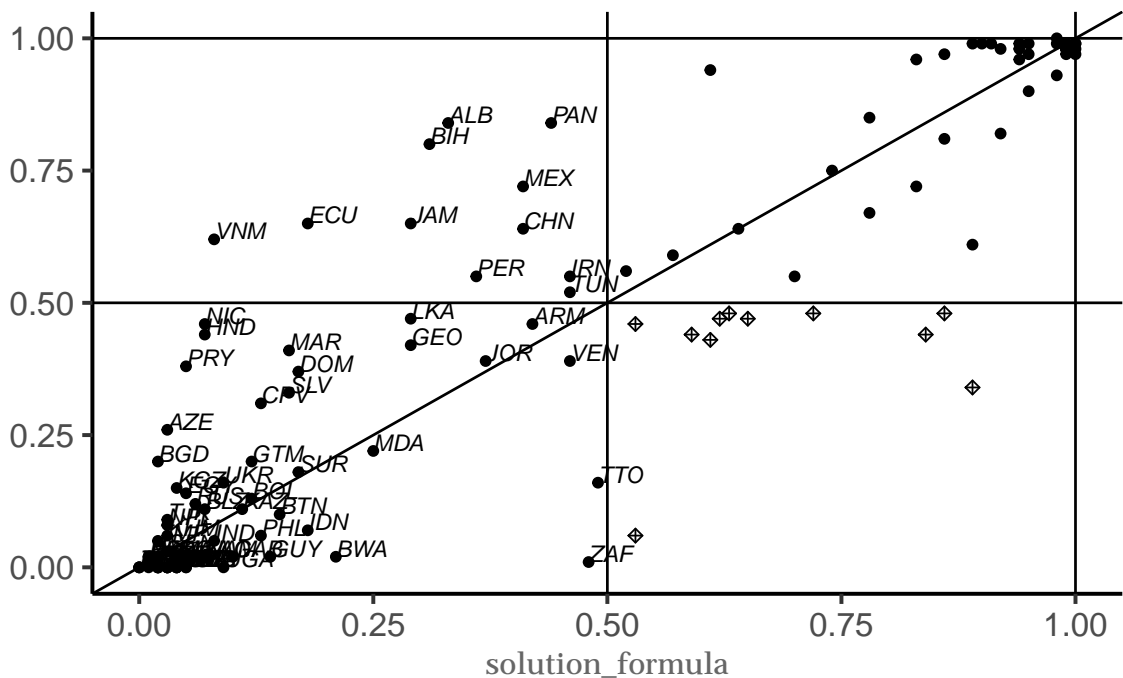
SUFFICIENCY PLOT

Cons.Suf: 0.844; Cov.Suf: 0.134; PRI: 0.373



SUFFICIENCY PLOT

Cons.Suf: 0.885; Cov.Suf: 0.855; PRI: 0.837



4. NECESSITY ANALYSIS FOR THE ABSENCE OF THE OUTCOME

Analyze necessary conditions for outcome ~Y using the superSubset function. Set inclusion cutoff to 0.908, depth to 2, coverage cutoff to 0.8 and RoN to 0.8.

```
SUIN_ny <- superSubset(data = PAYF,
                        outcome = "~HL",
                        conditions = conds,
```

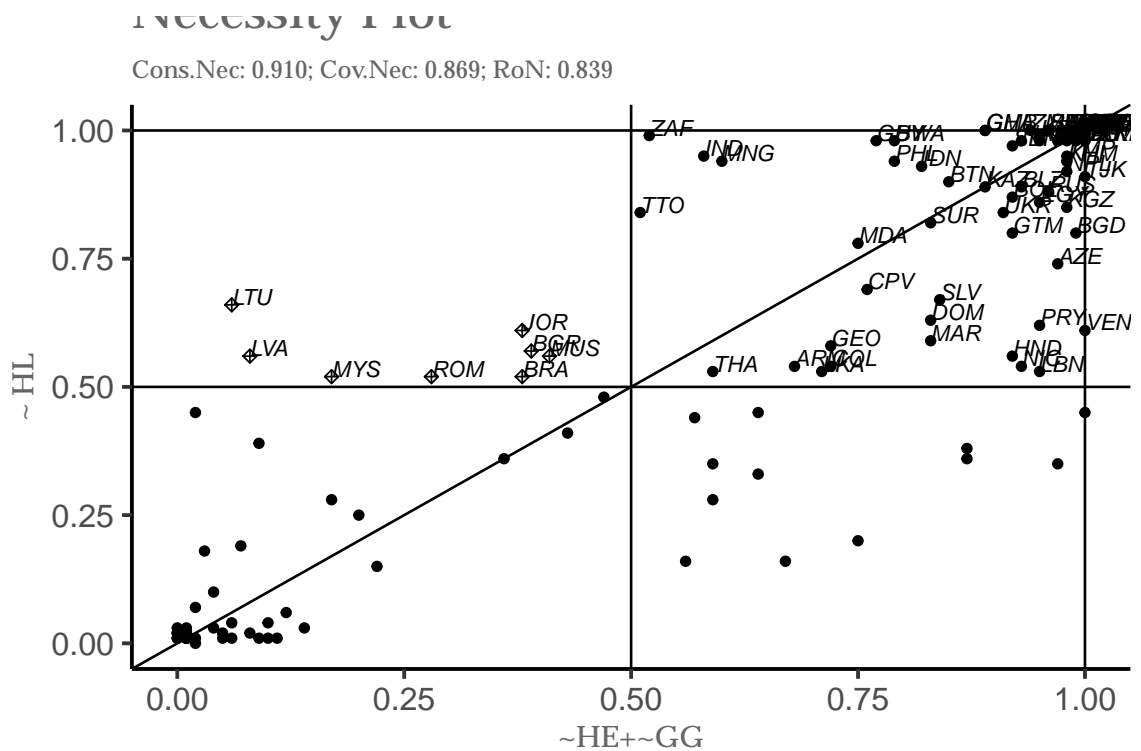
```
incl.cut = 0.908,
cov.cut = 0.8,
ron.cut = 0.8,
depth = 2)
```

```
SUIN_ny
```

```
##
##           inclN   RoN   covN
## -----
## 1 ~HE+~GG 0.910 0.839 0.869
## -----
```

Plot the results:

```
pimplot(data = PAYF,
         outcome = "HL",
         results = SUIN_ny,
         necessity = TRUE)
```



5. SUFFICIENCY ANALYSIS FOR THE ABSENCE OF THE OUTCOME

Truth Table

Create a truth table setting the inclusion cutoff to 0.9 and the number of cases needed to include a row in the analysis to 2.

```
TT_ny <- truthTable(data = PAYF,
                    outcome = "~HL",
                    conditions = conds,
                    incl.cut = 0.9,
                    n.cut = 2,
                    sort.by = c("OUT", "incl"),
                    complete = TRUE)
```

```
TT_ny
```

```

##
##   OUT: output value
##   n: number of cases in configuration
##   incl: sufficiency inclusion score
##   PRI: proportional reduction in inconsistency
##
##      HE GG AH HI HW   OUT    n   incl  PRI
## 19  1  0  0  1  0     1     2  0.960 0.827
##  5  0  0  1  0  0     1     4  0.954 0.892
## 11  0  1  0  1  0     1     7  0.954 0.908
## 25  1  1  0  0  0     1     2  0.953 0.803
##  3  0  0  0  1  0     1    30  0.951 0.929
##  1  0  0  0  0  0     1    16  0.950 0.926
##  7  0  0  1  1  0     1     2  0.947 0.849
## 20  1  0  0  1  1     1     2  0.946 0.691
## 22  1  0  1  0  1     1     2  0.935 0.791
##  4  0  0  0  1  1     1     4  0.934 0.781
## 12  0  1  0  1  1     1     6  0.912 0.752
## 24  1  0  1  1  1     0     2  0.894 0.490
## 28  1  1  0  1  1     0     4  0.806 0.405
## 32  1  1  1  1  1     0     5  0.650 0.175
## 30  1  1  1  0  1     0    36  0.285 0.055
## 17  1  0  0  0  0     ?     1  0.969 0.890
## 21  1  0  1  0  0     ?     1  0.963 0.855
## 13  0  1  1  0  0     ?     1  0.950 0.752
## 15  0  1  1  1  0     ?     1  0.940 0.755
##  6  0  0  1  0  1     ?     1  0.927 0.772
## 26  1  1  0  0  1     ?     1  0.910 0.611
## 14  0  1  1  0  1     ?     1  0.898 0.565
##  2  0  0  0  0  1     ?     0  -      -
##  8  0  0  1  1  1     ?     0  -      -
##  9  0  1  0  0  0     ?     0  -      -
## 10  0  1  0  0  1     ?     0  -      -
## 16  0  1  1  1  1     ?     0  -      -
## 18  1  0  0  0  1     ?     0  -      -
## 23  1  0  1  1  0     ?     0  -      -
## 27  1  1  0  1  0     ?     0  -      -
## 29  1  1  1  0  0     ?     0  -      -
## 31  1  1  1  1  0     ?     0  -      -

```

Logical Minimization

Produce the most parsimonious solution:

```

sol_nyp <- minimize(TT_ny,
                    details = TRUE,
                    include = "?")
sol_nyp

```

```

##
## M1: ~HE + ~GG*~AH + ~GG*~HI + (~HW) -> ~HL
## M2: ~HE + ~GG*~AH + ~GG*~HI + (~AH*~HI) -> ~HL
##
##
##      inclS  PRI  covS  covU  (M1)  (M2)
## -----
## 1      ~HE  0.905  0.877  0.832  0.029  0.033  0.129
## 2  ~GG*~AH  0.905  0.870  0.676  0.007  0.007  0.022
## 3  ~GG*~HI  0.927  0.897  0.398  0.021  0.021  0.033
## -----

```

```
## 4      ~HW  0.914  0.886  0.829  0.013  0.024
## 5  ~AH*~HI  0.918  0.878  0.332  0.004          0.014
## -----
##          M1  0.875  0.839  0.929
##          M2  0.882  0.848  0.919
```

Check the simplifying assumptions:

```
sol_nyp$SA
```

```
## $M1
##   HE GG AH HI HW
## 2  0  0  0  0  1
## 6  0  0  1  0  1
## 8  0  0  1  1  1
## 9  0  1  0  0  0
## 10 0  1  0  0  1
## 13 0  1  1  0  0
## 14 0  1  1  0  1
## 15 0  1  1  1  0
## 16 0  1  1  1  1
## 17 1  0  0  0  0
## 18 1  0  0  0  1
## 21 1  0  1  0  0
## 23 1  0  1  1  0
## 27 1  1  0  1  0
## 29 1  1  1  0  0
## 31 1  1  1  1  0
##
## $M2
##   HE GG AH HI HW
## 2  0  0  0  0  1
## 6  0  0  1  0  1
## 8  0  0  1  1  1
## 9  0  1  0  0  0
## 10 0  1  0  0  1
## 13 0  1  1  0  0
## 14 0  1  1  0  1
## 15 0  1  1  1  0
## 16 0  1  1  1  1
## 17 1  0  0  0  0
## 18 1  0  0  0  1
## 21 1  0  1  0  0
## 26 1  1  0  0  1
```

Produce the intermediate solution with the following directional expectations 0, 0, 0, 1, 0:

```
sol_nyi <- minimize(TT_ny,
                    details = TRUE,
                    include = "?",
                    dir.exp = c(0, 0, 0, 1, 0))
sol_nyi
```

```
##
## From C1P1:
##
## M1:   ~GG*~AH + ~GG*~HI + ~AH*~HW + ~HE*~GG*~HW + ~HE*~AH*HI -> ~HL
##
##           inclS  PRI  covS  covU
## -----
## 1      ~GG*~AH  0.905  0.870  0.676  0.010
## 2      ~GG*~HI  0.927  0.897  0.398  0.043
```

```

## 3      ~AH*~HW  0.920  0.894  0.735  0.042
## 4  ~HE*~GG*~HW  0.942  0.922  0.674  0.018
## 5  ~HE*~AH*HI  0.913  0.881  0.541  0.014
## -----
##              M1  0.887  0.854  0.893
##
##
## From C1P2:
##
## M1:      ~GG*~AH + ~GG*~HI + ~HE*~GG*~HW + ~HE*~AH*HI + ~AH*~HI*~HW -> ~HL
##
##              inclS  PRI  covS  covU
## -----
## 1      ~GG*~AH  0.905  0.870  0.676  0.026
## 2      ~GG*~HI  0.927  0.897  0.398  0.043
## 3  ~HE*~GG*~HW  0.942  0.922  0.674  0.018
## 4  ~HE*~AH*HI  0.913  0.881  0.541  0.063
## 5  ~AH*~HI*~HW  0.937  0.904  0.312  0.012
## -----
##              M1  0.893  0.860  0.863

```

Check the easy counterfactuals

```
sol_nyi$i.sol$C1P1$EC
```

```

##   HE GG AH HI HW
## 2  0  0  0  0  1
## 6  0  0  1  0  1
## 9  0  1  0  0  0
## 17 1  0  0  0  0
## 18 1  0  0  0  1
## 21 1  0  1  0  0
## 27 1  1  0  1  0

```

```
sol_nyi$i.sol$C1P2$EC
```

```

##   HE GG AH HI HW
## 2  0  0  0  0  1
## 6  0  0  1  0  1
## 9  0  1  0  0  0
## 17 1  0  0  0  0
## 18 1  0  0  0  1
## 21 1  0  1  0  0

```

Look at the PI chart

```
sol_nyi$PIchart
```

```

##
##           1  3  4  5  7  11 12 19 20 22 25
## ~HE      x  x  x  x  x  x  x  -  -  -  -
## ~HW      x  x  -  x  x  x  -  x  -  -  x
## ~GG*~AH  x  x  x  -  -  -  -  x  x  -  -
## ~GG*~HI  x  -  -  x  -  -  -  -  -  x  -
## ~AH*~HI  x  -  -  -  -  -  -  -  -  -  x

```

6. ENHANCED STANDARD ANALYSIS FOR THE ABSENCE OF THE OUTCOME

Assumptions contradicting necessity

Let's use the intermediate solution

From SUIN_ny, we know that the expression $HE+GG$ contradicts the statement of necessity.

Does any of the simplifying assumptions for the most parsimonious solution contradict the statement of necessity?

```
sol_nyp$SA
```

```
## $M1
##   HE GG AH HI HW
##  2  0  0  0  0  1
##  6  0  0  1  0  1
##  8  0  0  1  1  1
##  9  0  1  0  0  0
## 10  0  1  0  0  1
## 13  0  1  1  0  0
## 14  0  1  1  0  1
## 15  0  1  1  1  0
## 16  0  1  1  1  1
## 17  1  0  0  0  0
## 18  1  0  0  0  1
## 21  1  0  1  0  0
## 23  1  0  1  1  0
## 27  1  1  0  1  0
## 29  1  1  1  0  0
## 31  1  1  1  1  0
##
## $M2
##   HE GG AH HI HW
##  2  0  0  0  0  1
##  6  0  0  1  0  1
##  8  0  0  1  1  1
##  9  0  1  0  0  0
## 10  0  1  0  0  1
## 13  0  1  1  0  0
## 14  0  1  1  0  1
## 15  0  1  1  1  0
## 16  0  1  1  1  1
## 17  1  0  0  0  0
## 18  1  0  0  0  1
## 21  1  0  1  0  0
## 26  1  1  0  0  1
```

Create a new truth table which will set such rows to $OUT=0$, using the esa function

```
TT_ny_esa <- esa(TT_ny,
                 nec_cond = c("~HE+~GG"))
TT_ny_esa
```

```
##
##   OUT: output value
##   n: number of cases in configuration
##   incl: sufficiency inclusion score
##   PRI: proportional reduction in inconsistency
##
##   HE GG AH HI HW   OUT   n   incl  PRI
## 19  1  0  0  1  0     1     2  0.960 0.827
##  5  0  0  1  0  0     1     4  0.954 0.892
## 11  0  1  0  1  0     1     7  0.954 0.908
## 25  1  1  0  0  0     0     2  0.953 0.803
##  3  0  0  0  1  0     1    30  0.951 0.929
##  1  0  0  0  0  0     1    16  0.950 0.926
##  7  0  0  1  1  0     1     2  0.947 0.849
```

```

## 20  1  0  0  1  1    1    2  0.946 0.691
## 22  1  0  1  0  1    1    2  0.935 0.791
##  4  0  0  0  1  1    1    4  0.934 0.781
## 12  0  1  0  1  1    1    6  0.912 0.752
## 24  1  0  1  1  1    0    2  0.894 0.490
## 28  1  1  0  1  1    0    4  0.806 0.405
## 32  1  1  1  1  1    0    5  0.650 0.175
## 30  1  1  1  0  1    0   36  0.285 0.055
## 17  1  0  0  0  0    ?    1  0.969 0.890
## 21  1  0  1  0  0    ?    1  0.963 0.855
## 13  0  1  1  0  0    ?    1  0.950 0.752
## 15  0  1  1  1  0    ?    1  0.940 0.755
##  6  0  0  1  0  1    ?    1  0.927 0.772
## 26  1  1  0  0  1    0    1  0.910 0.611
## 14  0  1  1  0  1    ?    1  0.898 0.565
##  2  0  0  0  0  1    ?    0    -    -
##  8  0  0  1  1  1    ?    0    -    -
##  9  0  1  0  0  0    ?    0    -    -
## 10  0  1  0  0  1    ?    0    -    -
## 16  0  1  1  1  1    ?    0    -    -
## 18  1  0  0  0  1    ?    0    -    -
## 23  1  0  1  1  0    ?    0    -    -
## 27  1  1  0  1  0    0    0    -    -
## 29  1  1  1  0  0    0    0    -    -
## 31  1  1  1  1  0    0    0    -    -

```

Rerun the analysis of sufficiency producing the ENHANCED intermediate solution for ~Y with the following directional expectations: 0,0,0,1,0

```

sol_nyi_esa <- minimize(TT_ny_esa,
                        include = "?",
                        details = TRUE,
                        dir.exp = c(0,0,0,1,0))

```

```
sol_nyi_esa
```

```

##
## From C1P1:
##
## M1:    ~GG*~AH + ~GG*~HI + ~HE*~GG*~HW + ~HE*~AH*HI -> ~HL
##
##              inclS  PRI  covS  covU
## -----
## 1      ~GG*~AH  0.905  0.870  0.676  0.026
## 2      ~GG*~HI  0.927  0.897  0.398  0.043
## 3  ~HE*~GG*~HW  0.942  0.922  0.674  0.018
## 4  ~HE*~AH*HI  0.913  0.881  0.541  0.067
## -----
##              M1  0.894  0.862  0.851

```

Contradictory easy counterfactuals

Check if we are making contradictory easy counterfactuals Put them in an object named CEC

```

CEC <- intersect(rownames(sol_yi$i.sol$C1P1$EC),
                 rownames(sol_nyi$i.sol$C1P1$EC))

```

```
CEC
```

```
## character(0)
```

We have none

Simultaneous subset relations

Now check if one or more rows were included into the minimization for both outcome Y and $\sim Y$. Use the intersect command, create a new object SSR

```
SSR <- intersect(rownames(TT_y$tt)[TT_y$tt$OUT==1],
                 rownames(TT_ny$tt)[TT_ny$tt$OUT==1])
SSR
```

```
## [1] "20"
```

Row 20 is included in both logical minimization processes, however, use the following commands to check the PRI value:

```
TT_y$tt[20,] # notice the low PRI value
```

```
##   HE GG AH HI HW OUT n          incl          PRI cases
## 20  1  0  0  1  1   2 0.873479318734793 0.281105990783411 COL,THA
```

```
TT_ny$tt[20,] # PRI is much higher and much above 0.5
```

```
##   HE GG AH HI HW OUT n          incl          PRI cases
## 20  1  0  0  1  1   2 0.94566098945661 0.691244239631335 COL,THA
```

We see that while for outcome HL, PRI is very low, for outcome $\sim HL$, PRI is much better (0.69), so we keep it in the logical minimization.

Impossible remainders

The combination of four conditions never empirically occurs: $H_EDUG_GOV_AFF_HEAL*\sim H_INCEQ$, so let's assume that it is impossible. Avoid untenable assumptions on any logical remainder that contains the combination of these four conditions. Produce new ENHANCED intermediate solution for $\sim Y$:

```
TT_ny_esa <- esa(TT_ny,
                 nec_cond = "~HE+~GG",
                 untenable_LR = "~HE*GG*~AH*~HI")
TT_ny_esa
```

```
##
##   OUT: output value
##   n: number of cases in configuration
##   incl: sufficiency inclusion score
##   PRI: proportional reduction in inconsistency
##
##   HE GG AH HI HW  OUT  n  incl  PRI
## 19  1  0  0  1  0    1   2  0.960 0.827
##  5  0  0  1  0  0    1   4  0.954 0.892
## 11  0  1  0  1  0    1   7  0.954 0.908
## 25  1  1  0  0  0    0   2  0.953 0.803
##  3  0  0  0  1  0    1  30  0.951 0.929
##  1  0  0  0  0  0    1  16  0.950 0.926
##  7  0  0  1  1  0    1   2  0.947 0.849
## 20  1  0  0  1  1    1   2  0.946 0.691
## 22  1  0  1  0  1    1   2  0.935 0.791
##  4  0  0  0  1  1    1   4  0.934 0.781
## 12  0  1  0  1  1    1   6  0.912 0.752
## 24  1  0  1  1  1    0   2  0.894 0.490
## 28  1  1  0  1  1    0   4  0.806 0.405
## 32  1  1  1  1  1    0   5  0.650 0.175
## 30  1  1  1  0  1    0  36  0.285 0.055
## 17  1  0  0  0  0    ?   1  0.969 0.890
## 21  1  0  1  0  0    ?   1  0.963 0.855
## 13  0  1  1  0  0    ?   1  0.950 0.752
```

```
## 15  0  1  1  1  0  ?  1  0.940 0.755
##  6  0  0  1  0  1  ?  1  0.927 0.772
## 26  1  1  0  0  1  0  1  0.910 0.611
## 14  0  1  1  0  1  ?  1  0.898 0.565
##  2  0  0  0  0  1  ?  0  -      -
##  8  0  0  1  1  1  ?  0  -      -
##  9  0  1  0  0  0  0  0  -      -
## 10  0  1  0  0  1  0  0  -      -
## 16  0  1  1  1  1  ?  0  -      -
## 18  1  0  0  0  1  ?  0  -      -
## 23  1  0  1  1  0  ?  0  -      -
## 27  1  1  0  1  0  0  0  -      -
## 29  1  1  1  0  0  0  0  -      -
## 31  1  1  1  1  0  0  0  -      -
```

Produce the enhanced intermediate solution:

```
sol_nyi_esa <- minimize(TT_ny_esa,
                        details = TRUE,
                        include = "?",
                        dir.exp = c(0,0,0,1,0))
sol_nyi_esa
```

```
##
## From C1P1:
##
## M1:    ~GG*~AH + ~GG*~HI + ~HE*~GG*~HW + ~HE*~AH*HI -> ~HL
##
##              inclS  PRI  covS  covU
## -----
## 1      ~GG*~AH  0.905  0.870  0.676  0.026
## 2      ~GG*~HI  0.927  0.897  0.398  0.043
## 3  ~HE*~GG*~HW  0.942  0.922  0.674  0.018
## 4  ~HE*~AH*HI  0.913  0.881  0.541  0.067
## -----
##              M1  0.894  0.862  0.851
```

7. THEORY EVALUATION

Let us assume that according to our theory, good governance (GG) and affluent health system (AH) or low income inequality (~HI) lead to high life expectancy (HL)

Intersect theory with the most parsimonious solution:

```
TH <- theory.evaluation(theory = "GG*AH+~HI",
                        empirics = sol_yp,
                        outcome = "HL",
                        sol = 1)
TH
```

```
##
## CASES:
## *****
##
## Covered Most Likely (T*S and Y > 0.5) :
## -----
##
## Boolean Expression: GG*~HE*~HI + GG*~HI*HW + AH*GG*HE*HW
##
## Cases in the intersection/Total number of cases: 37 / 131 = 28.24 %
## Cases in the intersection/Total number of cases Y > 0.5: 37 / 52 = 71.15 %
```

```

##
## Case Names:
## AUS AUT BRB BEL CAN HRV CYP CZE DNK EST FIN FRA DEU GRC HUN ISL IRL ISR ITA JPN KOR LUX M
## -----
##
## Covered Least Likely (~T*S and Y > 0.5) :
## -----
##
## Boolean Expression: ~AH*HE*HI*HW + ~GG*HE*HI*HW
##
## Cases in the intersection/Total number of cases: 4 / 131 = 3.05 %
## Cases in the intersection/Total number of cases Y > 0.5: 4 / 52 = 7.69 %
##
## Case Names:
## ARG CHL CRI TUR
## -----
##
## Uncovered Most Likely (T*~S and Y > 0.5) :
## -----
##
## Boolean Expression: ~GG*~HI + HE*~HI*~HW + AH*GG*~HE*HI + AH*GG*HE*~HW
##
## Cases in the intersection/Total number of cases: 3 / 131 = 2.29 %
## Cases in the intersection/Total number of cases Y > 0.5: 3 / 52 = 5.77 %
##
## Case Names:
## ALB TUN VNM
## -----
##
## Uncovered Least Likely (~T*~S and Y > 0.5) :
## -----
##
## Boolean Expression: ~AH*~HE*HI + ~AH*HI*~HW + ~GG*~HE*HI + ~GG*HI*~HW
##
## Cases in the intersection/Total number of cases: 8 / 131 = 6.11 %
## Cases in the intersection/Total number of cases Y > 0.5: 8 / 52 = 15.38 %
##
## Case Names:
## BIH CHN ECU IRN JAM MEX PAN PER
## -----
##
## Inconsistent Most Likely (T*S and Y < 0.5) :
## -----
##
## Boolean Expression: GG*~HE*~HI + GG*~HI*HW + AH*GG*HE*HW
##
## Cases in the intersection/Total number of cases: 0 / 131 = 0 %
## Cases in the intersection/Total number of cases Y < 0.5: 0 / 79 = 0 %
##
## Case Names:
## No cases in this intersection
## -----
##
## Inconsistent Least Likely (~T*S and Y < 0.5) :
## -----
##
## Boolean Expression: ~AH*HE*HI*HW + ~GG*HE*HI*HW
##
## Cases in the intersection/Total number of cases: 4 / 131 = 3.05 %

```

```

## Cases in the intersection/Total number of cases Y < 0.5: 4 / 79 = 5.06 %
##
## Case Names:
## COL LBN MYS THA
## -----
##
## Consistent Most Likely (T*~S and Y < 0.5) :
## -----
##
## Boolean Expression: ~GG*~HI + HE*~HI*~HW + AH*GG*~HE*HI + AH*GG*HE*~HW
##
## Cases in the intersection/Total number of cases: 25 / 131 = 19.08 %
## Cases in the intersection/Total number of cases Y < 0.5: 25 / 79 = 31.65 %
##
## Case Names:
## ARM AZE BDI KHM CMR EGY ETH GEO IND IDN JOR KAZ KGZ LAO LBR MLI MDA PAK RUS LKA TJK TZA T
## -----
##
## Consistent Least Likely (~T*~S and Y < 0.5) :
## -----
##
## Boolean Expression: ~AH*~HE*HI + ~AH*HI*~HW + ~GG*~HE*HI + ~GG*HI*~HW
##
## Cases in the intersection/Total number of cases: 43 / 131 = 32.82 %
## Cases in the intersection/Total number of cases Y < 0.5: 43 / 79 = 54.43 %
##
## Case Names:
## AGO BGD BLZ BEN BTN BOL BWA BFA CPV TCD CIV DOM SLV GAB GMB GHA GTM GIN GUY HND KEN MDG M
## -----

```

8. ROBUSTNESS

Sensitivity ranges:

Find the raw consistency and the frequency cut sensitivity ranges (for Y):

```

rob.inclrange(
  data = PAYF,
  step = 0.01,
  max.runs = 20,
  outcome = "HL",
  conditions = conds,
  incl.cut = 0.84,
  n.cut = 1,
  include = "?"
)

```

```

## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## Raw Consistency T.: Lower bound 0.81 Threshold 0.84 Upper bound 0.84

```

```

rob.ncutrange(
  data = PAYF,
  step = 1,
  max.runs = 20,
  outcome = "HL",
  conditions = conds,

```

```
incl.cut = 0.84,
n.cut = 1,
include = "?"
)
```

```
## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## [1] "Searching for thresholds, this takes me a while for now, sorry..."
## N.Cut: Lower bound 1 Threshold 1 Upper bound 1
```

Load the raw data:

```
data("PAYR")
head(PAYR)
```

```
##      COUNTRY                REGION LIFEX EDUC  GOV  HEAL INCEQ  WEAL
## ALB  Albania          European Region  77.8  3.85 -0.23 -0.24 17.52  9569
## AGO  Angola            African Region  52.4  2.01 -1.07 -0.75 43.06  5669
## ARG  Argentina Region of the Americas  76.3  4.48 -0.30  0.16 31.52 18233
## ARM  Armenia          European Region  74.8  3.82 -0.26  0.17 12.74  7062
## AUS  Australia Western Pacific Region  82.8  5.56  1.60  1.38 16.82 41576
## AUT  Austria          European Region  81.5  5.43  1.57  1.88 14.44 43459
```

Creating the test solutions:

Alter consistency to 0.8 and inclusion cutoff to 2. Create a new object TS1

```
TS1 <- minimize(data = PAYF,
               outcome = "HL",
               conditions = conds,
               incl.cut = 0.8,
               n.cut = 2,
               include = "?",
               details = TRUE, show.cases = TRUE)
```

TS1

```
##
## M1: HE*HI + (HE*GG) -> HL
## M2: HE*HI + (GG*~HI) -> HL
##
##
##          inclS  PRI  covS  covU  (M1)  (M2)
## -----
## 1 HE*HI  0.809  0.606  0.353  0.049  0.049  0.188
## -----
## 2 HE*GG  0.874  0.828  0.820  0.034  0.515
## 3 GG*~HI 0.841  0.790  0.659  0.013          0.494
## -----
##          M1  0.849  0.789  0.869
##          M2  0.820  0.748  0.847
##
##          cases
## -----
## 1 HE*HI  CHN,PHL; COL,THA; ARG,LBN; CHL,CRI,MYS,TUR; BRA,HRV,ISR,USA,URY
## -----
## 2 HE*GG  JOR,TUN; CHL,CRI,MYS,TUR; AUS,AUT,BRB,BEL,BGR,CAN,CYP,CZE,DNK,EST,FIN,FRA,DEU,
##          BRA,HRV,ISR,USA,URY
## 3 GG*~HI  JOR,TUN; AUS,AUT,BRB,BEL,BGR,CAN,CYP,CZE,DNK,EST,FIN,FRA,DEU,GRC,HUN,ISL,IRL,I
## -----
```

Alter calibration for the condition HW, using the condition WEAL in the raw dataset and putting thresholds at 4000, 25000, and 45000

```
PAYF2 <- PAYF
PAYF2$HW <- calibrate(PAYR$WEAL,
                      type="fuzzy",
                      thresholds = c(4000,25000,45000),
                      logistic = TRUE,
                      idm = 0.95)
```

Create object called TS2. This should be the most parsimonious solution using parameters from the very first truth table (sufficiency analysis for the presence of the outcome)

```
TS2 <- minimize(data = PAYF2,
                outcome = "HL",
                conditions = conds,
                incl.cut = 0.84,
                n.cut = 1,
                include = "?",
                details = TRUE, show.cases = TRUE)
```

TS2

```
##
## M1: HE*GG*HI + HE*AH*HI + GG*AH*~HI -> HL
##
##          inclS  PRI  covS  covU
## -----
## 1  HE*GG*HI  0.865  0.715  0.304  0.080
## 2  HE*AH*HI  0.908  0.777  0.252  0.028
## 3  GG*AH*~HI  0.908  0.878  0.631  0.481
## -----
##          M1  0.885  0.837  0.813
##
##          cases
## -----
## 1  HE*GG*HI  CHL,CRI,MYS,TUR; BRA,HRV,URY; ISR,USA
## 2  HE*AH*HI  ARG,LBN; BRA,HRV,URY; ISR,USA
## 3  GG*AH*~HI  MNG,SRB; BRB,BGR,HUN,LVA,LTU,MNE,POL,ROM,SVK; AUS,AUT,BEL,CAN,CYP,CZE,DNK,E
## -----
```

Save the most parsimonious solution for the presence of the outcome as a new object IS:

```
IS <- sol_yp
```

Create the test set in a list:

```
TS <- list(TS1, TS2)
```

Calculate robustness fit parameters:

```
rob.fit(test_sol = TS,
        initial_sol = IS,
        outcome = "HL")

##          RF_cov RF_cons RF_SC_minTS RF_SC_maxTS
## Robustness_Fit  0.92  0.941  0.848  0.907
```

Identify types of robustness relevant cases and robustness case parameters:

```
rob.fit(test_sol = TS,
        initial_sol = IS,
        outcome = "HL")
```

```
## RF_cov RF_cons RF_SC_minTS RF_SC_maxTS
## Robustness_Fit 0.92 0.941 0.848 0.907
```

9. SMMR Y

Print the typical cases for each focal conjunct in the second sufficient term of the intermediate solution

```
typ_foc <- smmr(sol_yi,
  outcome = "HL",
  match = FALSE,
  cases = 2,
  term = 2)
```

```
typ_foc
```

```
## Typical Cases - Focal Conjunct HE :
```

```
## -----
## FocalConj Outcome CompConj Term UniqCov Best MostTypFC Rank ConsFC
## TUR 0.57 0.59 0.70 0.57 FALSE 0.47 FALSE 1 TRUE
## CHL 0.90 0.96 0.83 0.83 FALSE 0.29 FALSE 2 TRUE
## ISR 0.98 0.99 0.62 0.62 FALSE 0.40 FALSE 2 TRUE
## HRV 0.78 0.85 0.65 0.65 FALSE 0.49 FALSE 2 TRUE
## CRI 0.88 0.94 0.61 0.61 FALSE 0.51 FALSE 2 TRUE
```

```
## MostTypTerm
```

```
## TUR FALSE
## CHL FALSE
## ISR FALSE
## HRV FALSE
## CRI FALSE
```

```
##
```

```
## Typical Cases - Focal Conjunct HI :
```

```
## -----
## FocalConj Outcome CompConj Term UniqCov Best MostTypFC Rank ConsFC
## USA 0.91 0.93 1.00 0.91 FALSE 0.13 TRUE 1 TRUE
## HRV 0.65 0.85 0.78 0.65 FALSE 0.75 FALSE 1 TRUE
## ISR 0.62 0.99 0.96 0.62 FALSE 1.12 FALSE 1 TRUE
## CHL 0.97 0.96 0.83 0.83 FALSE 0.19 FALSE 2 FALSE
## URY 0.80 0.75 0.74 0.74 FALSE 0.36 FALSE 2 FALSE
```

```
## MostTypTerm
```

```
## USA TRUE
## HRV FALSE
## ISR FALSE
## CHL FALSE
## URY FALSE
```

```
##
```

```
## Typical Cases - Focal Conjunct HW :
```

```
## -----
## FocalConj Outcome CompConj Term UniqCov Best MostTypFC Rank ConsFC
## URY 0.74 0.75 0.80 0.74 FALSE 0.28 FALSE 1 TRUE
## CHL 0.83 0.96 0.90 0.83 FALSE 0.43 FALSE 1 TRUE
## CRI 0.61 0.94 0.88 0.61 FALSE 1.05 FALSE 1 TRUE
## HRV 0.84 0.85 0.65 0.65 FALSE 0.37 FALSE 2 TRUE
## ISR 0.96 0.99 0.62 0.62 FALSE 0.44 FALSE 2 TRUE
```

```
## MostTypTerm
```

```
## URY FALSE
## CHL FALSE
## CRI FALSE
## HRV FALSE
## ISR FALSE
```

Show the typical - IIR cases for each term, using the intermediate solution:

```
typ_iir_term <- smmr(results = sol_yi,
                    outcome = "HL",
                    match = TRUE,
                    cases = 6)

typ_iir_term

## Term HE*GG*HW :
## -----
##   Typical IIR UniqCov GlobUncov Best MostTyp ConsIIR
## 1     AUS AGO   TRUE      TRUE 0.02   TRUE   TRUE
## 2     CAN AGO   TRUE      TRUE 0.02   TRUE   TRUE
## 3     ISL AGO   TRUE      TRUE 0.02   TRUE   TRUE
## 4     NLD AGO   TRUE      TRUE 0.02   TRUE   TRUE
## 5     AUS BDI   TRUE      TRUE 0.02   TRUE   TRUE
##
## Term HE*HI*HW :
## -----
##   Typical IIR UniqCov GlobUncov Best MostTyp ConsIIR
## 1     USA AGO   TRUE      TRUE 0.20   TRUE   TRUE
## 2     USA BDI   TRUE      TRUE 0.20   TRUE   TRUE
## 3     USA TCD   TRUE      TRUE 0.20   TRUE   TRUE
## 4     USA ETH   TRUE      TRUE 0.22   TRUE   TRUE
## 7     USA MRT   TRUE      TRUE 0.23   TRUE   TRUE
##
## Term ~HE*GG*AH*~HI :
## -----
##   Typical IIR UniqCov GlobUncov Best MostTyp ConsIIR
## 1     SRB AGO   TRUE      TRUE 1.00   TRUE   TRUE
## 2     SRB BDI   TRUE      TRUE 1.00   TRUE   TRUE
## 4     SRB CIV   TRUE      TRUE 1.00   TRUE   TRUE
## 6     SRB NGA   TRUE      TRUE 1.00   TRUE   TRUE
## 11    SRB ZAF   TRUE      TRUE 1.03   TRUE   TRUE
```

10. SMMR $\sim Y$

Display the deviant cases coverage, using the intermediate solution:

```
dcov <- smmr(results = sol_nyi,
             outcome = "HL",
             match = FALSE,
             cases = 4)

dcov

## Deviant Coverage Cases :
## -----
##   Case SolMembership TT_HE TT_GG TT_AH TT_HI TT_HW TT_row_membership Outcome
## 7   MNG             0.47   0     1     1     0     0             0.53 0.94
## 3   GEO             0.36   0     1     1     1     0             0.64 0.58
## 4   LBN             0.39   1     0     1     1     1             0.61 0.53
## 8   MUS             0.29   1     1     0     0     1             0.59 0.56
## 9   MYS             0.17   1     1     0     1     1             0.82 0.52
## 5   LTU             0.06   1     1     1     0     1             0.76 0.66
## 10  ROM             0.28   1     1     1     0     1             0.72 0.52
## 1   BGR             0.25   1     1     1     0     1             0.61 0.57
## 6   LVA             0.09   1     1     1     0     1             0.58 0.56
## 2   BRA             0.38   1     1     1     1     1             0.53 0.52
##   Best MostDevCov ConstT
## 7 0.47           TRUE  TRUE
## 3 0.36           TRUE FALSE
```

```
## 4 0.39      TRUE FALSE
## 8 0.41      TRUE FALSE
## 9 0.18      TRUE FALSE
## 5 0.24      TRUE FALSE
## 10 0.28     FALSE FALSE
## 1 0.39     FALSE FALSE
## 6 0.42     FALSE FALSE
## 2 0.47      TRUE FALSE
```

Using the intermediate solution, show the best pairs of Deviant Coverage - IIR cases in each TT row:

```
dcov_iir <- smmr(results = sol_nyi,
  outcome = "HL",
  match = TRUE,
  cases = 4)
```

```
dcov_iir
```

```
## Matching Deviant Coverage-IIR Cases :
```

```
## -----
##      DevCov IIR TT_HE TT_GG TT_AH TT_HI TT_HW Best ConstTT_DCV
## 1      LBN ARG      1      0      1      1      1 1.58      FALSE
## 2      MYS CHL      1      1      0      1      1 0.90      FALSE
## 3      MYS CRI      1      1      0      1      1 1.32      FALSE
## 4      MYS TUR      1      1      0      1      1 1.75      FALSE
## 5      LTU JPN      1      1      1      0      1 0.82      FALSE
## 6      LTU AUS      1      1      1      0      1 0.83      FALSE
## 7      LTU ISL      1      1      1      0      1 0.83      FALSE
## 8      LTU NLD      1      1      1      0      1 0.83      FALSE
## 9      LTU ITA      1      1      1      0      1 0.83      FALSE
## 10     BRA ISR      1      1      1      1      1 1.43      FALSE
## 11     BRA USA      1      1      1      1      1 1.49      FALSE
## 12     BRA HRV      1      1      1      1      1 1.57      FALSE
## 13     BRA URY      1      1      1      1      1 1.67      FALSE
```

11. CLUSTER ~Y

We use the enhanced intermediate solution for the negated outcome

Perform cluster diagnostics for the enhanced intermediate solution with “REGION” as clusters and “COUNTRY” as units:

```
C_PAYF <- cluster(data = PAYF,
  result = sol_nyi_esa,
  outcome = "HL",
  unit_id = "COUNTRY",
  cluster_id = 'REGION',
  necessity = FALSE,
  wicons = FALSE)
```

```
C_PAYF
```

```
## Consistencies:
```

```
## -----
##                                     ~GG*~AH ~GG*~HI ~HE*~GG*~HW
## Pooled                             0.905  0.927  0.942
## Between African Region (33)        1.000  1.000  1.000
## Between Eastern Mediterranean Region (8) 0.893  0.976  0.977
## Between European Region (46)        0.831  0.865  0.877
## Between Region of the Americas (26)  0.790  1.000  0.865
## Between South-East Asian Region (8)  0.919  0.954  0.954
```

```

## Between Western Pacific Region (10)      0.815  0.826      0.864
##                                           ~HE*~AH*HI
## Pooled                                   0.913
## Between African Region (33)              0.997
## Between Eastern Mediterranean Region (8)  0.950
## Between European Region (46)            0.846
## Between Region of the Americas (26)     0.768
## Between South-East Asian Region (8)     1.000
## Between Western Pacific Region (10)     0.946
##
##
## Distances:
## -----
##                                           ~GG*~AH ~GG*~HI ~HE*~GG*~HW ~HE*~AH*HI
## From Between to Pooled  0.033  0.029      0.025      0.037
##
##
## Coverages:
## -----
##                                           ~GG*~AH ~GG*~HI ~HE*~GG*~HW
## Pooled                                   0.676  0.398      0.674
## Between African Region (33)             0.725  0.260      0.725
## Between Eastern Mediterranean Region (8)  0.838  0.734      0.688
## Between European Region (46)            0.313  0.751      0.480
## Between Region of the Americas (26)     0.784  0.110      0.693
## Between South-East Asian Region (8)     0.731  0.573      0.727
## Between Western Pacific Region (10)     0.754  0.524      0.703
##                                           ~HE*~AH*HI
## Pooled                                   0.541
## Between African Region (33)              0.672
## Between Eastern Mediterranean Region (8)  0.312
## Between European Region (46)            0.179
## Between Region of the Americas (26)     0.829
## Between South-East Asian Region (8)     0.410
## Between Western Pacific Region (10)     0.313

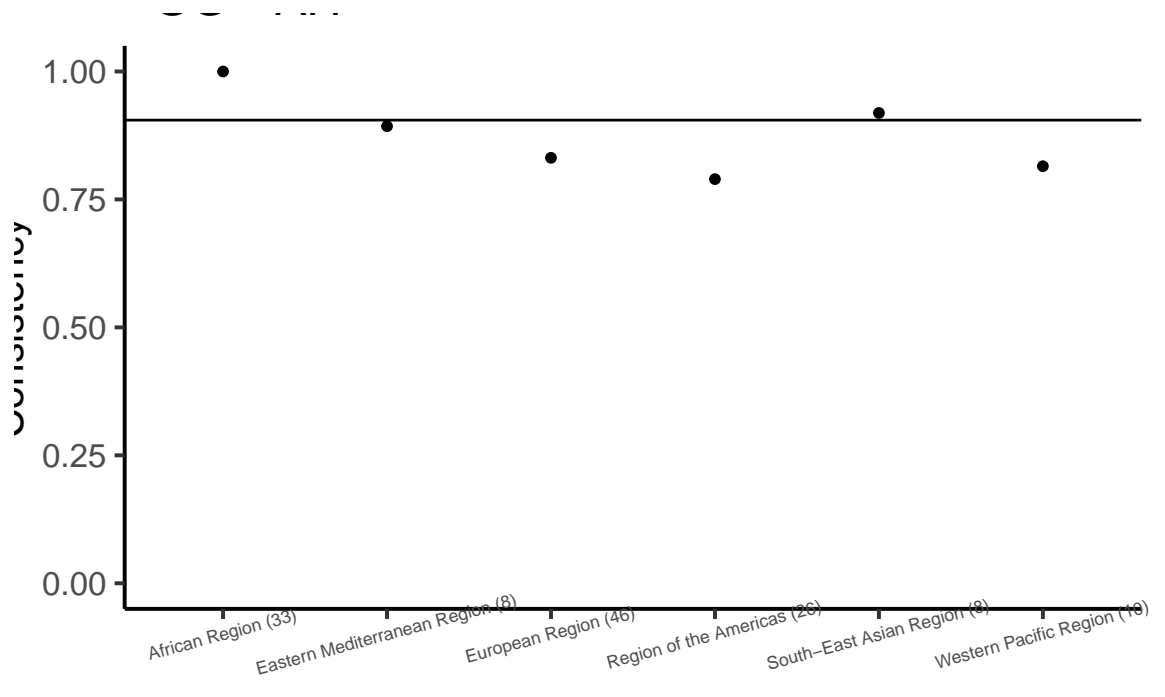
```

Plot between consistencies:

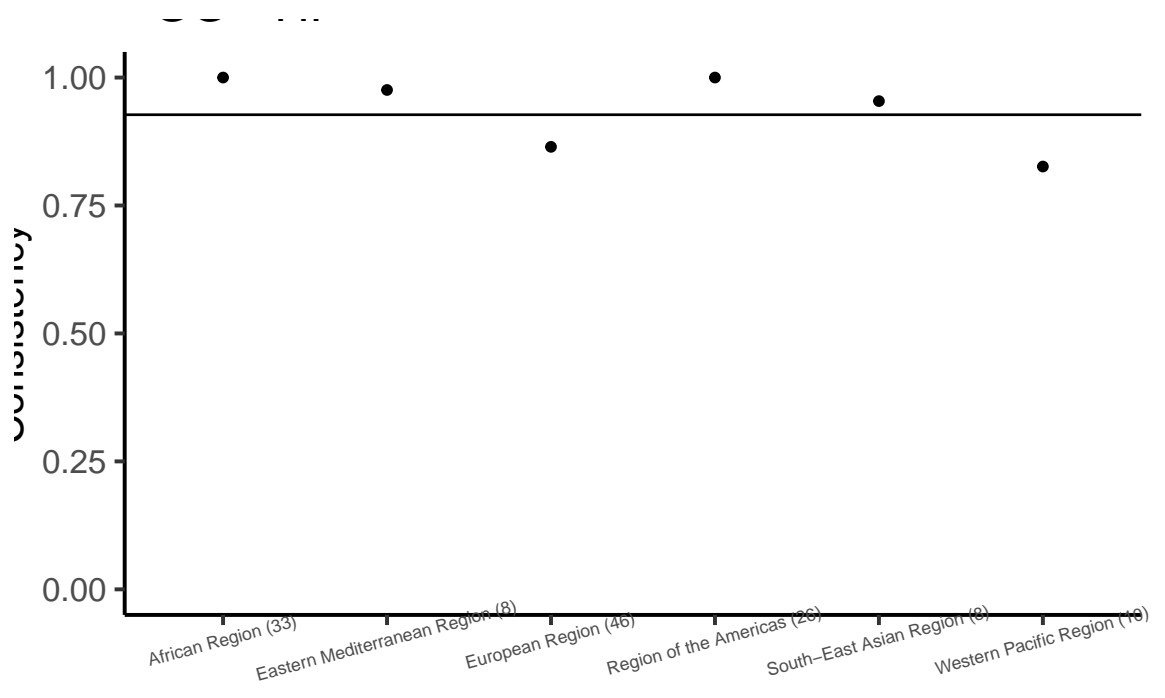
```

cluster.plot(C_PAYF,
             labs = TRUE,
             size = 7,
             angle = 15,
             wicons = FALSE)

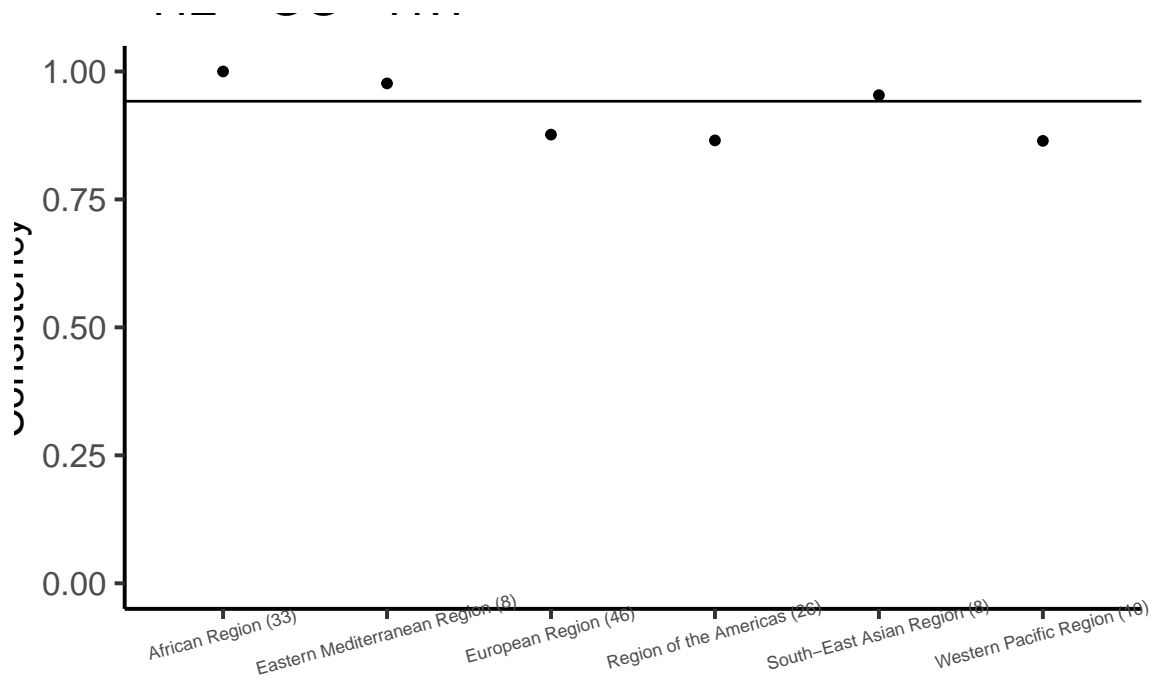
```



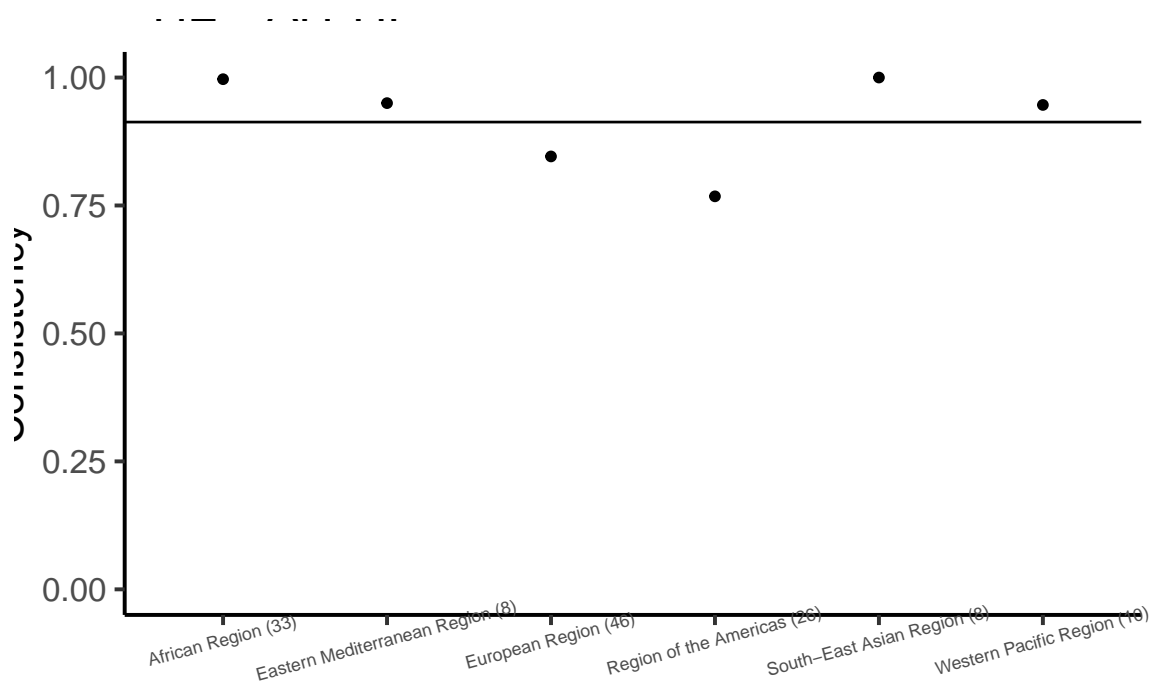
Clusters



Clusters



Clusters



Clusters